5. The analyzing method according to claim 3, wherein the functional analysis is performed by disruption of a gene or overexpression of a gene.

6. The analyzing method according to claim 1, wherein the industrial yeast is a brewing yeast.

7. The analyzing method according to claim 6, wherein the brewing yeast is a beer yeast.

8. The analyzing method according to claim 7, wherein the beer yeast is a bottom fermenting yeast.

9. A gene of the industrial yeast encoding an amino acid sequence having 70 to 97% identity to an amino acid sequence encoded by the gene of *Saccharomyces cerevisiae*, or consisting of a nucleotide sequence having 60 to 94% identity to the nucleotide sequence of the gene of *Saccharomyces cerevisiae*, which is obtained by the analyzing method according to any one of claims **1**-**8**.

10. A gene library comprising one or more of genes of the industrial yeast each of which encodes an amino acid sequence having 70 to 97% identity to an amino acid sequence encoded by the gene of *Saccharomyces cerevisiae*, or consists of a nucleotide sequence having 60 to 94% identity to the nucleotide sequence of the gene of *Saccharomyces cerevisiae*, which is obtained by the analyzing method according to any one of claim 1.

11. The gene library according to claim 10, wherein the gene of the industrial yeast is comprised in, consists of or has any nucleotide sequence selected from SEQ ID NOs:33 to 6236, SEQ ID NOs:166154 to 166181, SEQ ID NOs:166490 to 167042 and SEQ ID NOs:173125 to 174603.

12. A DNA array comprising one or more of DNAs, wherein each DNA is selected from at least one group of (1) to (4):

(1) DNA consisting of a nucleotide sequence of an open reading frame of the genome sequence of an industrial yeast which encodes an amino acid sequence having 70 to 97% identity to an amino acid sequence encoded by the gene of *Saccharomyces cerevisiae*, or a nucleotide sequence complementary to the above nucleotide sequence, or a nucleotide sequence of continuous 10 or more nucleotides selected from the above nucleotide sequences;

(2) DNA consisting of a nucleotide sequence of the genome sequence of an industrial yeast other than from open reading frames which consists of a nucleotide sequence having 60 to 94% identity to the nucleotide sequence of the gene of *Saccharomyces cerevisiae*, or a nucleotide sequence complementary to the above nucleotide sequence, or a nucleotide sequence of continuous 10 or more nucleotides selected from the above nucleotide sequences;

(3) DNA having a nucleotide sequence of any of SEQ ID NOs:166490 to 167042, or DNA having a nucleotide sequence of any of SEQ ID NOs:167043 to 173124; and

(4) DNA having a nucleotide sequence of any of SEQ ID NOs:173125 to 174603, or DNA having a nucleotide sequence of any of SEQ ID NOs:174604 to 190810.

13. The DNA array according to claim 12 comprising DNAs wherein at least one DNA is selected from every group of (1) to (4).

14. The DNA array according to claim 12, wherein the DNAs of (1) is comprised in, consists of or has any nucleotide sequence selected from SEQ ID NOs:33 to 6236, SEQ ID NOs:166154 to 166181, SEQ ID NOs:6237 to 75336 and SEQ ID NOs:166182 to 166489.

15. The DNA array according to any one of claim 12, which further comprises, in addition to at least one group of DNAs selected from (1) to (4), DNAs of the following (5) and/or (6):

(5) DNA consisting of a nucleotide sequence of an open reading frame of the genome sequence of an industrial yeast which encodes an amino acid sequence having identity of more than 97% to an amino acid sequence encoded by the gene of *Saccharomyces cerevisiae*, or a nucleotide sequence complementary to the above nucleotide sequence, or a nucleotide sequence of continuous 10 or more nucleotides selected from the above nucleotide sequences; and

(6) DNA consisting of a nucleotide sequence of the genome sequence of an industrial yeast other than from open reading frames which consists of a nucleotide sequence having identity of more than 94% to the nucleotide sequence of the gene of *Saccharomyces cerevisiae*, or a nucleotide sequence complementary to the above nucleotide sequence, or a nucleotide sequence of continuous 10 or more nucleotides selected from the above nucleotide sequences, and optionally DNAs of the following (5') and/or (6'):

(5') DNA consisting of a nucleotide sequence which contains mismatch of 1 or more base(s) to the DNA of (5), or a nucleotide sequence complementary to the above nucleotide sequence; and

(6') DNA consisting of a nucleotide sequence which contains mismatch of 1 or more base(s) to the DNA of (6), or a nucleotide sequence complementary to the above nucleotide sequence.

16. The DNA array according to claim 15, wherein the DNAs of (5) has a nucleotide sequence of any one of SEQ ID NOs:75337 to 82784, or SEQ ID NOs:82785 to 166153.

17. The DNA array according to any one of claim 12, which comprises, in addition to at least one group of DNAs selected from (1) to (4), DNAs selected from at least one of (7) to (10):

(7) DNA consisting of a nucleotide sequence which contains mismatch of 1 or more base(s) to the DNA of (1), or a nucleotide sequence complementary to the above nucleotide sequence;

(8) DNA consisting of a nucleotide sequence which contains mismatch of 1 or more base(s) to the DNA of (2), or a nucleotide sequence complementary to the above nucleotide sequence;

(9) DNA consisting of a nucleotide sequence which contains mismatch of 1 or more base(s) to the DNA of (3), or a nucleotide sequence complementary to the above nucleotide sequence; and

(10) DNA consisting of a nucleotide sequence which contains mismatch of 1 or more base(s) to the DNA of (4), or a nucleotide sequence complementary to the above nucleotide sequence.

18. The DNA array according to claim 17, which comprises, in addition to at least one group of DNAs selected